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#2 OIPE

RAW SEQUENCE LISTING

DATE: 02/10/2002

PATENT APPLICATION: US/09/996,561

TIME: 16:02:31

Input Set : N:\Crf3\RULE60\09996561.raw

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1 <110> APPLICANT: YOKOYAMA, KEIICHI
 2 NAKAMURA, NAMI
 3 MIWA, TETSUYA
 4 SEGURO, KATSUYA
 5 <120> TITLE OF INVENTION: PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE
 6 <130> FILE REFERENCE: 0010-0937-0
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/996,561
 8 <141> CURRENT FILING DATE: 2001-11-30
 9 <150> PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/448,310
 W--> 10 <151> PRIOR FILING DATE: CURRENT FILING DATE: 1999-11-24
 12 <150> PRIOR APPLICATION NUMBER: 09/109,063
 13 <151> PRIOR FILING DATE: 1998-07-02
 14 <160> NUMBER OF SEQ ID NOS: 62
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 331
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Artificial Sequence
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Description of Artificial
 23 Sequence:TRANSGLUTAMINASE
 24 <400> SEQUENCE: 1
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 26 1 5 10 15
 27 Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn
 28 20 25 30
 29 Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg
 30 35 40 45
 31 Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys
 32 50 55 60
 33 Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu
 34 65 70 75 80
 35 Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn
 36 85 90 95
 37 Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val
 38 100 105 110
 39 Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu
 40 115 120 125
 41 Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser
 42 130 135 140
 43 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala
 44 145 150 155 160
 45 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn

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46          165          170          175
47  Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg
48          180          185          190
49  Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg
50          195          200          205
51  Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg
52          210          215          220
53  Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile
54  225          230          235          240
55  Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr
56          245          250          255
57  Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp
58          260          265          270
59  Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met
60          275          280          285
61  His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp
62          290          295          300
63  Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn
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75 <222> LOCATION: (1)..(993)
76 <223> OTHER INFORMATION: IDENTIFICATION METHOD: S
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79  Asp Ser Asp Asp Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met
80  1          5          10          15
81  cca gat cca tat cgt cca tct tat ggt cgt gct gaa act gtt gtt aat 96
82  Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn
83          20          25          30
84  aat tat att cgt aaa tgg caa caa gtt tat tct cat cgt gat ggt cgt 144
85  Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg
86          35          40          45
87  aaa caa caa atg act gaa gaa caa cgt gaa tgg ctg tct tat ggt tgc 192
88  Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys
89          50          55          60
90  gtt ggt gtt act tgg gtt aac tct ggt cag tat ccg act aac cgt ctg 240
91  Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu
92          65          70          75          80
93  gca ttc gct tcc ttc gat gaa gat cgt ttc aag aac gaa ctg aag aac 288
94  Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn
95          85          90          95

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96      ggt cgt ccg cgt tct ggt gaa act cgt gct gaa ttc gaa ggt cgt gtt      336
97      Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val
98              100                      105                      110
99      gct aag gaa tcc ttc gat gaa gag aaa ggc ttc cag cgt gct cgt gaa      384
100     Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu
101              115                      120                      125
102     gtt gct tct gtt atg aac cgt gct cta gag aac gct cat gat gaa tct      432
103     Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser
104              130                      135                      140
105     gct tac ctg gat aac ctg aag gaa ctg gct aac ggt aac gat gct      480
106     Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala
107     145                      150                      155                      160
108     ctg cgt aac gaa gat gct cgt tct ccg ttc tac tct gct ctg cgt aac      528
109     Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn
110              165                      170                      175
111     act ccg tcc ttc aaa gaa cgt aac ggt ggt aac cat gat ccg tct cgt      576
112     Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg
113              180                      185                      190
114     atg aaa gct gtt atc tac tct aaa cat ttc tgg tct ggt cag gat aga      624
115     Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg
116              195                      200                      205
117     tct tct tct gct gat aaa cgt aaa tac ggt gat ccg gat gca ttc cgt      672
118     Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg
119              210                      215                      220
120     ccg gct ccg ggt act ggt ctg gta gac atg tct cgt gat cgt aac atc      720
121     Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile
122     225                      230                      235                      240
123     ccg cgt tct ccg act tct ccg ggt gaa ggc ttc gtt aac ttc gat tac      768
124     Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr
125              245                      250                      255
126     ggt tgg ttc ggt gct cag act gaa gct gat gct gat aag act gta tgg      816
127     Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp
128              260                      265                      270
129     acc cat ggt aac cat tac cat gct ccg aac ggt tct ctg ggt gct atg      864
130     Thr His Gly Asn His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met
131              275                      280                      285
132     cat gta tac gaa tct aaa ttc cgt aac tgg tct gaa ggt tac tct gac      912
133     His Val Tyr Glu Ser Lys Phe Arg Asn Trp Ser Glu Gly Tyr Ser Asp
134              290                      295                      300
135     ttc gat cgt ggt gct tac gtt atc acc ttc att ccg aaa tct tgg aac      960
136     Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn
137     305                      310                      315                      320
138     act gct ccg gac aaa gtt aaa cag ggt tgg ccg      993
139     Thr Ala Pro Asp Lys Val Lys Gln Gly Trp Pro
140              325                      330
142 <210> SEQ ID NO: 3
143 <211> LENGTH: 1519
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial Sequence

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146 <220> FEATURE:
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149 <222> LOCATION: (87)..(1082)
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152      ggtatcgatt agtaaggagg tttaaa atg gat tct gac gat cgt gtt act cca 113
153                      Met Asp Ser Asp Arg Val Thr Pro
154                      1                      5
155      cca gct gaa cca ctg gat cgt atg cca gat cca tat cgt cca tct tat 161
156      Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr
157      10                      15                      20                      25
158      ggt cgt gct gaa act gtt gtt aat aat tat att cgt aaa tgg caa caa 209
159      Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln
160                      30                      35                      40
161      gtt tat tct cat cgt gat ggt cgt aaa caa caa atg act gaa gaa caa 257
162      Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln
163                      45                      50                      55
164      cgt gaa tgg ctg tct tat ggt tgc gtt ggt gtt act tgg gtt aac tct 305
165      Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser
166                      60                      65                      70
167      ggt cag tat ccg act aac cgt ctg gca ttc gct tcc ttc gat gaa gat 353
168      Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp
169      75                      80                      85
170      cgt ttc aag aac gaa ctg aag aac ggt cgt ccg cgt tct ggt gaa act 401
171      Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr
172      90                      95                      100                      105
173      cgt gct gaa ttc gaa ggt cgt gtt gct aag gaa tcc ttc gat gaa gag 449
174      Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu
175                      110                      115                      120
176      aaa ggc ttc cag cgt gct cgt gaa gtt gct tct gtt atg aac cgt gct 497
177      Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala
178                      125                      130                      135
179      cta gag aac gct cat gat gaa tct gct tac ctg gat aac ctg aag aag 545
180      Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys
181      140                      145                      150
182      gaa ctg gct aac ggt aac gat gct ctg cgt aac gaa gat gct cgt tct 593
183      Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser
184      155                      160                      165
185      ccg ttc tac tct gct ctg cgt aac act ccg tcc ttc aaa gaa cgt aac 641
186      Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn
187      170                      175                      180                      185
188      ggt ggt aac cat gat ccg tct cgt atg aaa gct gtt atc tac tct aaa 689
189      Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys
190                      190                      195                      200
191      cat ttc tgg tct ggt cag gat aga tct tct tct gct gat aaa cgt aaa 737
192      His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala Asp Lys Arg Lys
193                      205                      210                      215
194      tac ggt gat ccg gat gca ttc cgt ccg gct ccg ggt act ggt ctg gta 785

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195   Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val
196           220           225           230
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198   Asp Met Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly
199           235           240           245
200   gaa ggc ttc gtt aac ttc gat tac ggt tgg ttc ggt gct cag act gaa 881
201   Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu
202           250           255           260           265
203   gct gat gct gat aag act gta tgg acc cat ggt aac cat tac cat gct 929
204   Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala
205           270           275           280
206   ccg aac ggt tct ctg ggt gct atg cat gta tac gaa tct aaa ttc cgt 977
207   Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg
208           285           290           295
209   aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc 1025
210   Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile
211           300           305           310
212   acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag 1073
213   Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln
214           315           320           325
215   ggt tgg ccg taatgaaagc ttggatctct aattactgga cttcacacag 1122
216   Gly Trp Pro
217           330
218   actaaaatag acatatctta tattatgtga ttttgtgaca tttcctagat gtgaggtgga 1182
219   ggtgatgtat aaggtagatg atgacctctt acgccggacg catcgtggcc ggcatacccg 1242
220   gcgccacagg tgcggttgct ggcgcctata tcgccgacat caccgatggg gaagatcggg 1302
221   ctgcgcactt cgggctcatg agcgccttgtt tcggcgtggg tatggtggca ggccccgtgg 1362
222   ccgggggact gttgggcgcc atctccttgc atgcaccatt ccttgccggc gcggtgctca 1422
223   acggcctcaa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcgtc 1482
224   gagagcccg ctaatgagcg ggcttttttt tcagctg 1519
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229 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
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236 <211> LENGTH: 41
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
241 <400> SEQUENCE: 5
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244 <210> SEQ ID NO: 6
245 <211> LENGTH: 41
246 <212> TYPE: DNA

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VERIFICATION SUMMARY

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